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<170> FastSEQ for Windows Version 3.0

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SEQUENCE INFORMATION

BASB027 Polynucleotide and Polypeptide Sequences

SEQ ID NO:1

Moraxella catarrhalis BASB027 polynucleotide sequence from strain ATCC 43617

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SEQ ID NO:2

Moraxella catarrhalis BASB027 polypeptide sequence deduced from the
polynucleotide sequence of SEQ ID NO:1

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VSENQLADGVKALYATGNFSDVQVYHQEGRIIYQVTERPLIAEINFEGNRLIPKEGLQEG
LKNAGLAVGQPLKQATVQMIETELTNQYISQGYNTEITVKQTMLDGNRVKLDMTFAEGK
PARVVDINIIGNQHFSDADLIDVLAIKDNKINPLSKADRYTQEKLVTSLLENLRAKYLNAG
FVRFEIKDAKLNINEDKNRIFVEISLHEGEQYRFGQTQFLGNLTYTQAELEALLKFKAEE
GFSQAMLEQTTNNISTKFGDDGYYYAQIRPVTRINDESRTVDVEYYIDPVHPVYVRRINF
TGNFKTQDEVLRREMRQLEGALASNQKIQLSRARLMRTGFFKHVTVDTRPVPNSPDQVDV
NFVVEEQPSGSSTIAAGYSQSGGVTFQFDVSQNNFMGTGKHVNASFRRSETREVYSLGMT
NPYFTVNGVSQSLSGYYRKT KYDNKNI SNYVLD SYGGSLSYGYPIDENQRI SFGLNADNT
KLHGGRFMGISNVKQLMADGGKIQVDNNGIPDFKHDTTYNAILGWNYSLLDRPVFPTQG
MSHSVLDLTVGFQKTHQKVYVQGNIRPFIKKSVLRGYAKLGYGNLFPYENFYAGGYGS
VRGYDQSSSLGPRSQAYLTARRGQQTTLGEVVGGNALATFGSELILPLPFKGDWIDQVRPV
IFIEGGQVFDTTGMDKQTDLTQFKDPQATAEQNAKAANRPLLTDQDKQLRYSAGVGATWY
TPIGPLSISYAKPLNKKQNDQTDTVQFQIGSVF

SEQ ID NO:3

Moraxella catarrhalis BASB027 polynucleotide sequence from strain ATCC 43617

ATGCGTAATTCATATTTTAAAGGTTTTTCAGGTCAGTGCAATGACAATGGCTGTCATGATG
GTAATGTCAACTCATGCACAAGCGGCGGATTTTATGGCAAATGACATTACCATCACAGGA
CTACAGCGAGTGACCATTGAAAGCTTACAAAGCGTGCTGCCGTTTTCGCTTGGGTCAAGTG
GTGAGCGAAAACCAGTTGGCTGATGGTGTCAAAGCACTTTATGCAACAGGCAATTTTTCA
GATGTGCAAGTCTATCATCAAGAAGGGCGTATCATCTATCAGGTAACCGAAAGGCCGTTA
ATCGCTGAGATTAATTTTGAGGGCAATCGCTTAATTCCAAAAGAAGGTCTACAAGAAGGG
CTAAAAAATGCTGGCTTAGCTGTGGGTCAACCACTAAAACAAGCCACAGTACAGATGATC
GAAACCGAGCTTACCAATCAATATATATCACAAGGCTATTATAATACCGAAATTACTGTC
AAACAGACGATGCTTGATGGTAATCGTGTTAAGCTTGATATGACCTTTGCTGAAGGTAAA
CCTGCACGGGTGGTTGATATTAATATCATTGGCAATCAGCATTTTAGCGATGCAGATTTG
ATTGATGTGCTTGCGATTAAGGATAATAAAATCAATCCACTGTCTAAAGCTGACCGTTAT
ACTCAAGAAAAGCTGGTGACCAGTTTAGAGAATTTGCGTGCTAAATATCTCAATGCAGGG
TTTGTGCGTTTTGAGATTAAAGATGCTAAGCTTAATATTAATGAAGATAAAAACCGTATC
TTTGTGAGATTTTATTGCATGAAGGTGAGCAATATCGCTTTGGACAGACACAGTTTTTG
GGTAATTTAACTTATACTCAAGCAGAACTTGAGGCACTGCTTAAATTCAAAGCAGAAGAA

GGGTTTTACAAGCCATGCTTGAGCAAACAACAACAATATCAGTACCAAATTTGGTGAC
 GATGGCTATTATTATGCTCAAATCCGTCCTGTAAACACGCATTAAATGATGAAAGTCGTACG
 GTTGATGTGGAATATTATATTGACCTGTACACCCTGTCTATGTACGCCGTATTAATTTT
 ACAGGTAACCTTTAAGACCCAAGATGAAGTACTCCGTCGTGAGATGCGACAACCTTGAAGGT
 GCGTTGGCATCTAATCAAAAAATCCAGCTGTCTCGTGCACGCTTGATGCGGACTGGGTTT
 TTAAACATGTTACCGTTGATACTCGTCCAGTACCCAACCTCACCTGATCAGGTTGATGTA
 AATTTTGTGGTTGAAGAACAACCTTCAGGATCATCAACCATCGCAGCAGGCTACTCTCAA
 AGTGGTGGTGTAACTTTTCAATTTGATGTTTCTCAAATAACTTTATGGGTACAGGTAAG
 CACGTCAATGCTTCGTTTTCTCGCTCTGAGACCCGTGAGGTGTATAGTTTGGGTATGACC
 AACCATACTTTACCGTAAATGGCGTCTCGCAAAGCTTGAGTGGCTACTATCGTAAACC
 AAGTATGATAACAAGAACATTAGTAATTATGTAATTGATTCTTATGGTGGCTCATTAGC
 TATGGATATCCAATTGATGAAAATCAACGCATAAGCTTTGGTCTGAATGCTGACAATACC
 AAGCTTCATGGCGGTTCGTTTTATGGGCATTAGTAATGTCAAGCAGCTGATGGCAGATGGT
 GGCAAATTCAGTGGATAATAATGGCATTCTGATTTTAAAGCATGATTACACAACCTAC
 AATGCCATTTTGGGGTGGAAATTATTCAAGTCTAGATCGCCCTGTATTTCCAACCCAAGGC
 ATGAGTCATTCTGTAGATTTGACGGTTGGTTTTGGTGATAAACTCATCAAAAAGTGGTT
 TATCAAGGCAATATCTATCGCCATTTATCAAAAATCAGTCTTGCGTGATACGCCAAG
 TTAGGCTATGGCAATAATTTACCATTTTATGAAAATTTCTATGCAGGCGGCTATGGTTCG
 GTTCGTGGCTATGATCAATCCTCTTTGGGTCCACGCTCACAAGCCTATTTGACAGCTCGT
 CGTGGTCAACAAACCACACTAGGAGAGGTTGTTGGTGGTAATGCTTTGGCAACTTTCGGC
 AGTGAGCTGATTTTACCTTTGCCATTTAAAGGTGATTGGATAGATCAGGTGCGTCCAGTG
 ATATTCATTGAGGGCGGTTCAGGTTTTGATACAACAGGTATGGATAAACAAACCATTGAT
 TTAACCCAATTTAAAGACCCACAAGCAACAGCTGAACAAAATGCAAAGCAGCCAATCGC
 CCGCTACTAACCCAAGATAAACAGTTGCGTTATAGTGCTGGTGTGGTGCAACTTGGTAT
 ACGCCCATTTGGTCTTTTATCTATTAGCTATGCCAAGCCATTGAATAAAAAACAAATGAT
 CAGACCGATACGGTACAGTTCAGATTGGTAGTGTCTTTTAA

SEQ ID NO:4

Moraxella catarrhalis BASB027 polypeptide sequence deduced from the
 polynucleotide sequence of SEQ ID NO:3

MRNSYFKGFQVSAMTMAVMMVMSTHAQAADFMANDITITGLQRVTIESLQSVLPFRLGQV
 VSENQLADGVKALYATGNFSDVQVYHQEGRIIYQVTERPLIAEINFEGNRLIPKEGLQEG
 LKNAGLAVGQPLKQATVQMIETELTNQYISQGYNTEITVKQTMLDGNNRVKLDMTFAEGK
 PARVVDINIIGNQHFSADLIDVLAIKDNKINPLSKADRYTQEKLVTSLENLRKAYLNAG
 FVRFEIKDAKLNINEDKNRIFVEISLHEGEQYRFGQTQFLGNLTYTQAELEALLKFKAEE
 GFSQAMLEQTTNNISTKFGDDGYYYAQIRPVTRINDESRTVDVEYYIDPVHPVYVRRINF
 TGNFKTQDEVLRREMRQLEGALASNQKIQLSRARLMRTGFFKHVTVDTRPVNPSPDQVDV
 NFVVEEQPSGSSTIAAGYSQSGGVTFQFDVSQNNFMGTGKHVNASFRRSETREVYSLGMT
 NPYFTVNGVSQSLSGYYRKT KYDNKNISNYVLDSYGGSLSYGYPIDENQRISFGLNADNT
 KLHGGFRMGISNVKQLMADGGKIQVDNNGIPDFKHDTTYNAILGWNYSLLDRPVFPQTQG
 MSHSVDLTVGFGDKTHQKVYQGNIRPFIKKSVLRGYAKLGYGNLPPFYENFYAGGYGS
 VRGYDQSSSLGPRSQAYLTARRGQQTTLGEVVGGNALATFGSELILPLPKGDWIDQVRPV
 IFIEGGQVFDTTGMDKQTDILTQFKDPQATAEQNAKAANRPLLTQDKQLRYSAGVGATWY

TPIGPLSISYAKPLNKKQNDQTDTVQFQIGSVF

SEQ ID NO:5

ACT ATA GGG CAC GCG TG

SEQ ID NO:6

CCT GCG TTT GTT TGA TTG AG

SEQ ID NO:7

AAG GGC CCA ATT ACG CAG AGG GGA TCC ACA GGA CTA CAG CGA GTG
ACC ATT GAA AGC TTA C

SEQ ID NO:8

AAG GGC CCA ATT ACG CAG AGG GTC GAC TTA TTA AAA GAC ACT ACC
AAT CTG GAA CTG TAC CGT ATC G

SEQ ID NO:9

CYAKPLNKKQNDQTD

SEQ ID NO:10

YLTARRGQQTTLGEVVC

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Figure 2 : Alignment of the BASB027 polynucleotide sequences.

Identity to SeqID No:1 is indicated by a dot.

	*	20	*	40	*	
Seqid1 :	ATGCGTAATTCATATTTTAAAGGTTTTTCAGGTCAGTGCAATGACAATGGC :					50
Seqid3 : :					50
		60	*	80	*	100
Seqid1 :	TGTCATGATGGTAATGTCAACTCATGCACAAGCGCGGATTTTATGGCAA :					100
Seqid3 : :					100
	*	120	*	140	*	
Seqid1 :	ATGACATTACCATCACAGGACTACAGCGAGTGACCATTGAAAGCTTACAA :					150
Seqid3 :G..... :					150
		160	*	180	*	200
Seqid1 :	AGCGTGCTGCCGTTTCGCTTGGGTCAAGTGGTGAGCGAAAACAGTTGGC :					200
Seqid3 :GCA..... :					200
	*	220	*	240	*	
Seqid1 :	TGATGGTGTCAAAGCACTTTATGCAACAGGCAATTTTTCAGATGTGCAAG :					250
Seqid3 : :					250
		260	*	280	*	300
Seqid1 :	TCTATCATCAAGAAGGGCGTATCATCTATCAGGTAACCGAAAGGCCGTTA :					300
Seqid3 : :					300
	*	320	*	340	*	
Seqid1 :	ATCGCTGAGATTAATTTTGAGGGCAATCGCTTAATTCCAAAGAAGGTCT :					350
Seqid3 : :					350

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360 * 380 * 400
Seqid1 : ACAAGAAGGGCTAAAAAATGCTGGCTTAGCTGTGGGTCAACCACTAAAAC : 400
Seqid3 : : 400

* 420 * 440 *
Seqid1 : AAGCCACAGTACAGATGATCGAAACCGAGCTTACCAATCAATATATATCA : 450
Seqid3 : : 450

460 * 480 * 500
Seqid1 : CAAGGCTATTATAATACCGAAATTACTGTCAAACAGACGATGCTTGATGG : 500
Seqid3 : : 500

* 520 * 540 *
Seqid1 : TAATCGTGTTAAGCTTGATATGACCTTTGCTGAAGGTAAACCTGCACGGG : 550
Seqid3 : : 550

560 * 580 * 600
Seqid1 : TGGTTGATATTAATATCATTGGCAATCAGCATTTTAGCGATGCAGATTTG : 600
Seqid3 : : 600

* 620 * 640 *
Seqid1 : ATTGATGTGCTTGCGATTAAGGATAATAAAATCAATCCACTGTCTAAAGC : 650
Seqid3 : : 650

660 * 680 * 700
Seqid1 : TGACCGTTTACTCAAGAAAAGCTGGTGACCAGTTTAGAGAATTTGCGTG : 700
Seqid3 : : 700

* 720 * 740 *
Seqid1 : CTAAATATCTCAATGCAGGGTTTGTGCGTTTTGAGATTAAAGATGCTAAG : 750

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Seqid3 : : 750

760 * 780 * 800
Seqid1 : CTTAATATTAATGAAGATAAAAACCGTATCTTTGTTGAGATTTTCATTGCA : 800
Seqid3 : : 800

* 820 * 840 *
Seqid1 : TGAAGGTGAGCAATATCGCTTTGGACAGACACAGTTTTTGGGTAATTTAA : 850
Seqid3 : : 850

860 * 880 * 900
Seqid1 : CTTATACTCAAGCAGAACTTGAGGCACTGCTTAAATTCAAAGCAGAAGAA : 900
Seqid3 : : 900

* 920 * 940 *
Seqid1 : GGGTTTTCAAGCCATGCTTGAGCAAACAACAATATCAGTACCAA : 950
Seqid3 : : 950

960 * 980 * 1000
Seqid1 : ATTTGGTGACGATGGCTATTATTATGCTCAAATCCGTCCTGTAACACGCA : 1000
Seqid3 : : 1000

* 1020 * 1040 *
Seqid1 : TTAATGATGAAAGTCGTACGGTTGATGTGGAATATTATATTGACCCTGTA : 1050
Seqid3 : : 1050

1060 * 1080 * 1100
Seqid1 : CACCCTGTCTATGTACGCCGTATTAATTTTACAGGTAACTTTAAGACCCA : 1100
Seqid3 : : 1100

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          *          1120          *          1140          *
Seqid1  : AGATGAAGTACTCCGTCGTGAGATGCGACAACTTGAAGGTGCGTTGGCAT : 1150
Seqid3  : ..... : 1150

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          1160          *          1180          *          1200
Seqid1  : CTAATCAAAAAATCCAGCTGTCTCGTGCACGCTTGATGCGGACTGGGTTT : 1200
Seqid3  : ..... : 1200

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          *          1220          *          1240          *
Seqid1  : TTAAACATGTTACCGTTGATACTCGTCCAGTACCCAACTCACCTGATCA : 1250
Seqid3  : ..... : 1250

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          1260          *          1280          *          1300
Seqid1  : GGTTGATGTAAATTTTGTGGTTGAAGAACAACCTTCAGGATCATCAACCA : 1300
Seqid3  : ..... : 1300

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          *          1320          *          1340          *
Seqid1  : TCGCAGCAGGCTACTCTCAAAGTGGTGGTGTAACCTTTTCAATTTGATGTT : 1350
Seqid3  : ..... : 1350

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          1360          *          1380          *          1400
Seqid1  : TCTCAAATAACTTTATGGGTACAGGTAAGCACGTCAATGCTTCGTTTTTC : 1400
Seqid3  : ..... : 1400

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          *          1420          *          1440          *
Seqid1 : TCGCTCTGAGACCCGTGAGGTGTATAGTTTGGGTATGACCAACCCATACT : 1450
Seqid3 : ..... : 1450

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          1460          *          1480          *          1500
Seqid1  : TTACCGTAAATGGCGTCTCGCAAAGCTTGAGTGGCTACTATCGTAAAACC : 1500
Seqid3  : ..... : 1500

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* 1520 * 1540 *
Seqid1 : AAGTATGATAACAAGAACATTAGTAATTATGTACTTGATTCTTATGGTGG : 1550
Seqid3 : : 1550

1560 * 1580 * 1600
Seqid1 : CTCATTAAGCTATGGATATCCAATTGATGAAAATCAACGCATAAGCTTTG : 1600
Seqid3 : : 1600

* 1620 * 1640 *
Seqid1 : GTCTGAATGCTGACAATACCAAGCTTCATGGCGGTCGTTTTATGGGCATT : 1650
Seqid3 : : 1650

1660 * 1680 * 1700
Seqid1 : AGTAATGTCAAGCAGCTGATGGCAGATGGTGGCAAAATTCAAGTGGATAA : 1700
Seqid3 : : 1700

* 1720 * 1740 *
Seqid1 : TAATGGCATTCTGATTTTAAGCATGATTACACAACCTACAATGCCATTT : 1750
Seqid3 : : 1750

1760 * 1780 * 1800
Seqid1 : TGGGGTGAATTATTCAAGTCTAGATCGCCCTGTATTTCCAACCCAAGGC : 1800
Seqid3 : : 1800

* 1820 * 1840 *
Seqid1 : ATGAGTCATTCTGTAGATTTGACGGTTGGTTTTGGTGATAAACTCATCA : 1850
Seqid3 : : 1850

1860 * 1880 * 1900
Seqid1 : AAAAGTGTTTATCAAGGCAATATCTATCGCCCATTTATCAAAAAATCAG : 1900

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Seqid3 : : 1900

* 1920 * 1940 *

Seqid1 : TCTTGCGTGGATACGCCAAGTTAGGCTATGGCAATAATTTACCATTTTAT : 1950

Seqid3 : : 1950

1960 * 1980 * 2000

Seqid1 : GAAAATTTCTATGCAGGCGGCTATGGTTCGGTTCGTGGCTATGATCAATC : 2000

Seqid3 : : 2000

* 2020 * 2040 *

Seqid1 : CTCTTTGGGTCCACGCTCACAAGCCTATTTGACAGCTCGTCGTGGTCAAC : 2050

Seqid3 : : 2050

2060 * 2080 * 2100

Seqid1 : AAACCACACTAGGAGAGGTTGTTGGTGGTAATGCTTTGGCAACTTTCGGC : 2100

Seqid3 : : 2100

* 2120 * 2140 *

Seqid1 : AGTGAGCTGATTTTACCTTTGCCATTTAAAGGTGATTGGATAGATCAGGT : 2150

Seqid3 : : 2150

2160 * 2180 * 2200

Seqid1 : GCGTCCAGTGATATTCATTGAGGGCGGTCAGGTTTTTGATACAACAGGTA : 2200

Seqid3 : : 2200

* 2220 * 2240 *

Seqid1 : TGGATAAAACAAACCATTGATTTAACCCAATTTAAAGACCCACAAGCAACA : 2250

Seqid3 : : 2250

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2260 * 2280 * 2300
Seqid1 : GCTGAACAAAATGCAAAAGCAGCCACTCGCCCGCTACTAACCCAAGATAA : 2300
Seqid3 : : 2300

* 2320 * 2340 *
Seqid1 : ACAGTTGCGTTATAGTGCTGGTGTGGTGCAACTTGGTATACGCCCATTG : 2350
Seqid3 : : 2350

2360 * 2380 * 2400
Seqid1 : GTCCTTTATCTATTAGCTATGCCAAGCCATTGAATAAAAAACAAAATGAT : 2400
Seqid3 : : 2400

* 2420 * 2440
Seqid1 : CAGACCGATACGGTACAGTTCCAGATTGGTAGTGTCTTTTAA : 2442
Seqid3 : : 2442

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Figure 3 : Alignment of the BASB027 polypeptide sequences.

Identity to SeqID No:2 is indicated by a dot.

```

                *           20           *           40           *
Seqid2 : MRNSYFKGFQVSAMTMVMMVMSTHAQAADFMANDITITGLQRTIESLQ : 50
Seqid4 : .....A..... : 50

                60           *           80           *           100
Seqid2 : SVLPFRLGQVVSENQLADGVKALYATGNFSDVQVYHQEGRIIYQVTERPL : 100
Seqid4 : .....A..... : 100

                *           120           *           140           *
Seqid2 : IAEINFEGNRLIPKEGLQEGLKNAGLAVGQPLKQATVQMIETELTNQYIS : 150
Seqid4 : ..... : 150

                160           *           180           *           200
Seqid2 : QGYNTEITVKQTMLDGNRVKLDMTFAEGKPARVVDINIIGNQHFSDADL : 200
Seqid4 : ..... : 200

                *           220           *           240           *
Seqid2 : IDVLAIKDNKINPLSKADRYTQEKLVTSLENLRAKYLNAGFVRFEIKDAK : 250
Seqid4 : ..... : 250

                260           *           280           *           300
Seqid2 : LNINEDKNRIFVEISLHEGEQYRFGQTQFLGNLTYTQAELEALLKFKAAEE : 300
Seqid4 : ..... : 300

                *           320           *           340           *
Seqid2 : GFSQAMLEQTTNNISTKFGDDGYYYAQIRPVTRINDESRTVDVEYYIDPV : 350
Seqid4 : ..... : 350
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360 * 380 * 400
Seqid2 : HPVYVRRINFTGNFKTQDEVLRREMRQLEGALASNQKIQLSRARLMRTGF : 400
Seqid4 : : 400

* 420 * 440 *
Seqid2 : FKHVTVDTRPVNPDQVDVNFVVEEQPSGSSTIAAGYSQSGGVTFQFDV : 450
Seqid4 : : 450

460 * 480 * 500
Seqid2 : SQNNFMGTGKHVNASFRRSETREVYSLGMTNPYFTVNGVSQSLSGYYRKT : 500
Seqid4 : : 500

* 520 * 540 *
Seqid2 : KYDNKNISNYVLDSYGGSLSYGYPIDENQRISFGLNADNTKLHGGRFMGI : 550
Seqid4 : : 550

560 * 580 * 600
Seqid2 : SNVKQLMADGGKIQVDNNGIPDFKHDTTYNAILGWNYSSLDRPVFPTQG : 600
Seqid4 : : 600

* 620 * 640 *
Seqid2 : MSHSVDLTVGFGDKTHQKVYQGNIIYRPFIKKSVLRGYAKLGYGNNLPFY : 650
Seqid4 : : 650

660 * 680 * 700
Seqid2 : ENFYAGGYGSVRGYDQSSLGPRSQAYLTARRGQOTTLGEVVGGNALATFG : 700
Seqid4 : : 700

* 720 * 740 *
Seqid2 : SELILPLPFKGDWIDQVRPVIFIEGGQVFDTTGMDKQTIDLTQFKDPQAT : 750

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Seqid4 : : 750

760

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Seqid2 : AEQNAKAAANRPLLTDKQLRYSAGVGATWYTPIGPLSISYAKPLNKKQND : 800

Seqid4 : : 800

*

Seqid2 : QTDTVQFQIGSVF : 813

Seqid4 : : 813

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Figure 4: Coomassie stained SDS-PAGE of purified BASB027 protein.

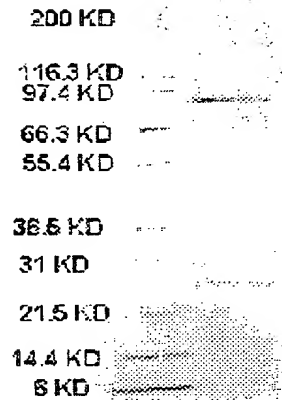
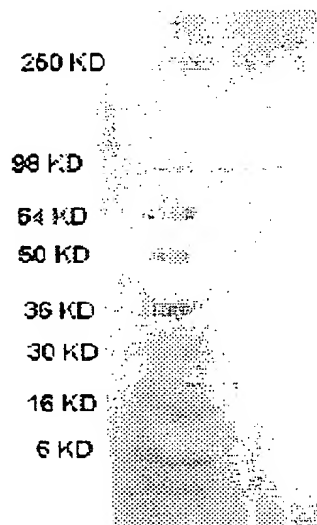
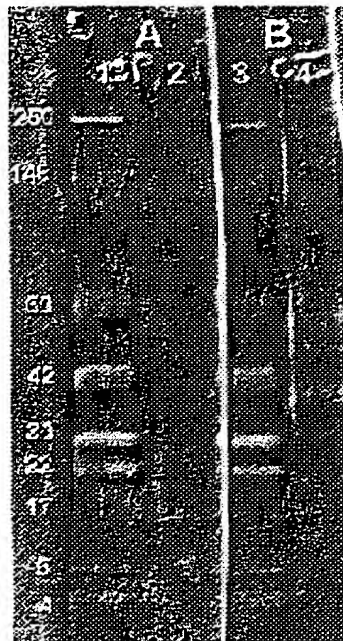


Figure 5: Western blot with tera-His antibody of purified BASB027 protein.



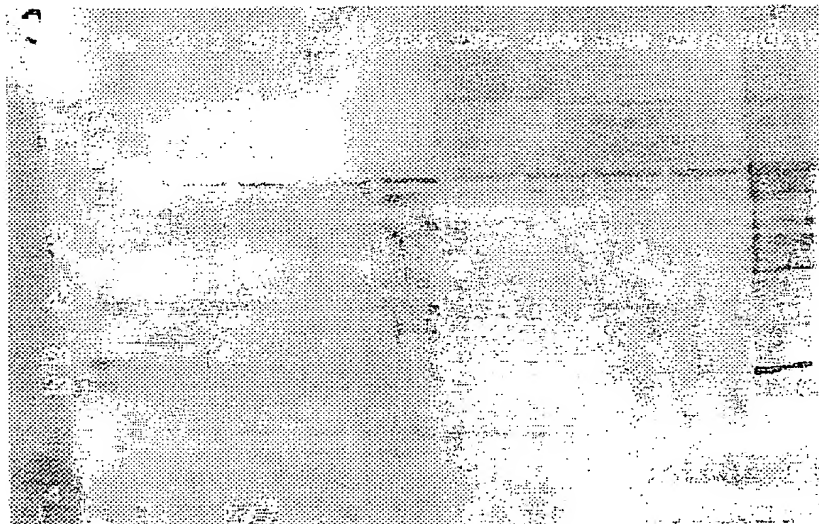
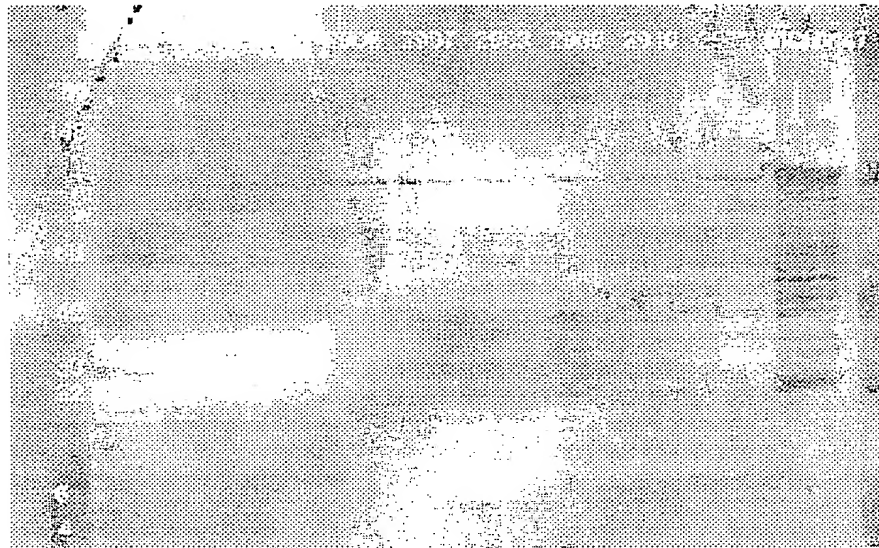
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Figure 6: Western blot of purified BASB027 protein with the corresponding anti-recombinant protein sera. Panel A: pre-immune serum. Panel B: immune serum.



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Figure 7: Western blot of whole cell lysates of 16 strains of *M. catarrhalis* using pooled sera against the BASB027 protein (sera was diluted 1:2000).



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Figure 8: Western blot of purified recombinant BASB027 with corresponding anti-peptide sera. Lanes 2 and 3 non immune sera. Lanes 1 and 4 immune sera.

